

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:52:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174038.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10174038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174038_1.fastq.gz SRR10174038_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:52:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,666,154
Mapped reads	1,624,324 / 97.49%
Unmapped reads	41,830 / 2.51%
Mapped paired reads	1,624,324 / 97.49%
Mapped reads, first in pair	813,828 / 48.84%
Mapped reads, second in pair	810,496 / 48.64%
Mapped reads, both in pair	1,597,528 / 95.88%
Mapped reads, singletons	26,796 / 1.61%
Secondary alignments	0
Supplementary alignments	159,729 / 9.59%
Read min/max/mean length	30 / 133 / 127.93
Duplicated reads (estimated)	1,200,659 / 72.06%
Duplication rate	62.53%
Clipped reads	639,165 / 38.36%

2.2. ACGT Content

Number/percentage of A's	58,062,274 / 30.22%
Number/percentage of C's	37,429,955 / 19.48%
Number/percentage of T's	57,920,672 / 30.15%
Number/percentage of G's	38,708,839 / 20.15%
Number/percentage of N's	2,163 / 0%

GC Percentage	39.63%
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2.3. Coverage

Mean	0.0621
Standard Deviation	1.0343

2.4. Mapping Quality

Mean Mapping Quality	53.06
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2.5. Insert size

Mean	1,117,698.69
Standard Deviation	9,917,797.07
P25/Median/P75	144 / 200 / 287

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	2,004,686
Insertions	21,876
Mapped reads with at least one insertion	1.29%
Deletions	43,752
Mapped reads with at least one deletion	2.63%
Homopolymer indels	42.46%

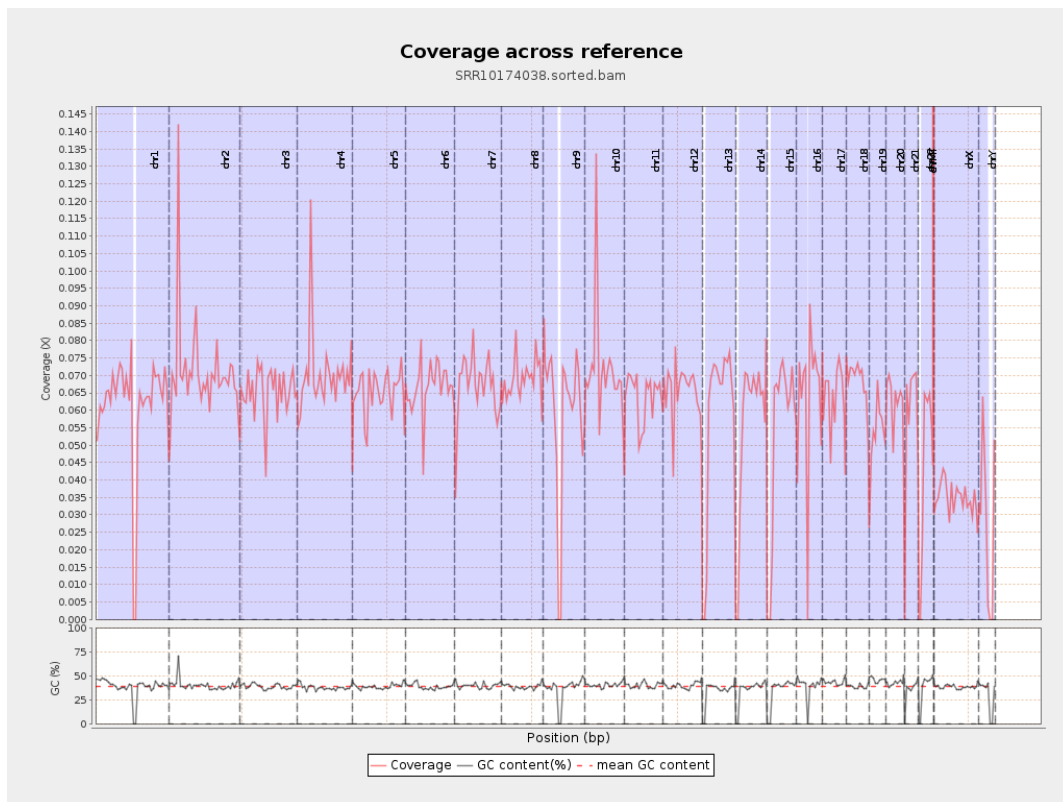
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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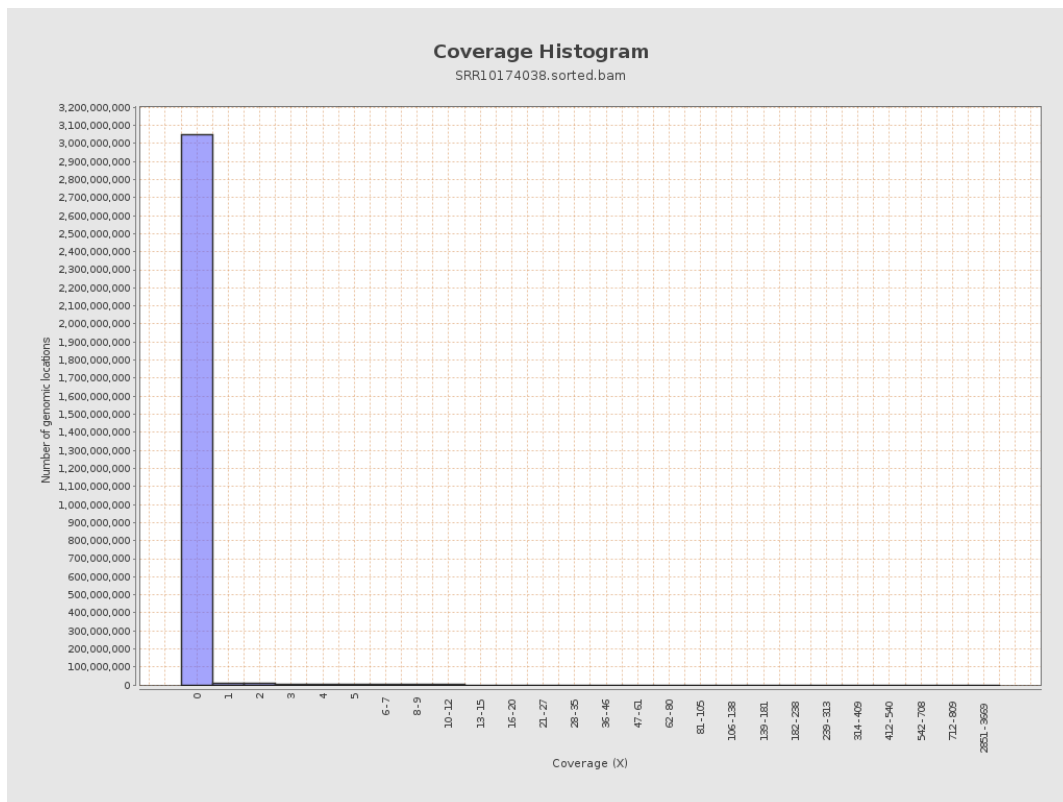
		bases	coverage	deviation
chr1	249250621	15306738	0.0614	0.8255
chr2	243199373	17344953	0.0713	2.6381
chr3	198022430	12927372	0.0653	0.6902
chr4	191154276	13381728	0.07	0.8603
chr5	180915260	11802155	0.0652	0.6947
chr6	171115067	11444976	0.0669	0.741
chr7	159138663	10733614	0.0674	0.8283
chr8	146364022	10105962	0.069	0.8857
chr9	141213431	8304838	0.0588	0.7821
chr10	135534747	9734042	0.0718	0.9498
chr11	135006516	8593787	0.0637	0.6847
chr12	133851895	8781083	0.0656	0.6962
chr13	115169878	6627184	0.0575	0.6571
chr14	107349540	5955368	0.0555	0.6416
chr15	102531392	5519085	0.0538	0.6166
chr16	90354753	5718559	0.0633	0.7654
chr17	81195210	5078136	0.0625	0.6943
chr18	78077248	5383389	0.0689	0.9337
chr19	59128983	3206017	0.0542	0.6747
chr20	63025520	3934559	0.0624	0.6729
chr21	48129895	2796150	0.0581	0.8205
chr22	51304566	2182660	0.0425	0.5863
chrMT	16571	357589	21.5792	19.2437
chrX	155270560	5417123	0.0349	0.5062

chrY	59373566	1596840	0.0269	0.5662
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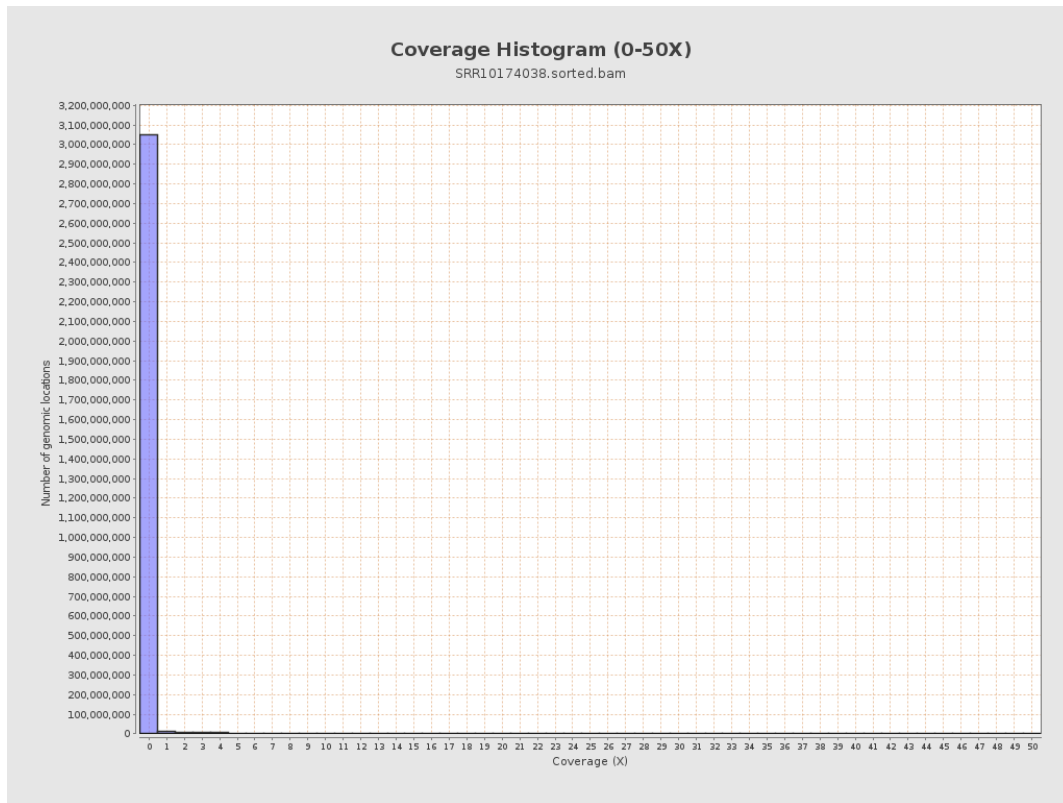
3. Results : Coverage across reference



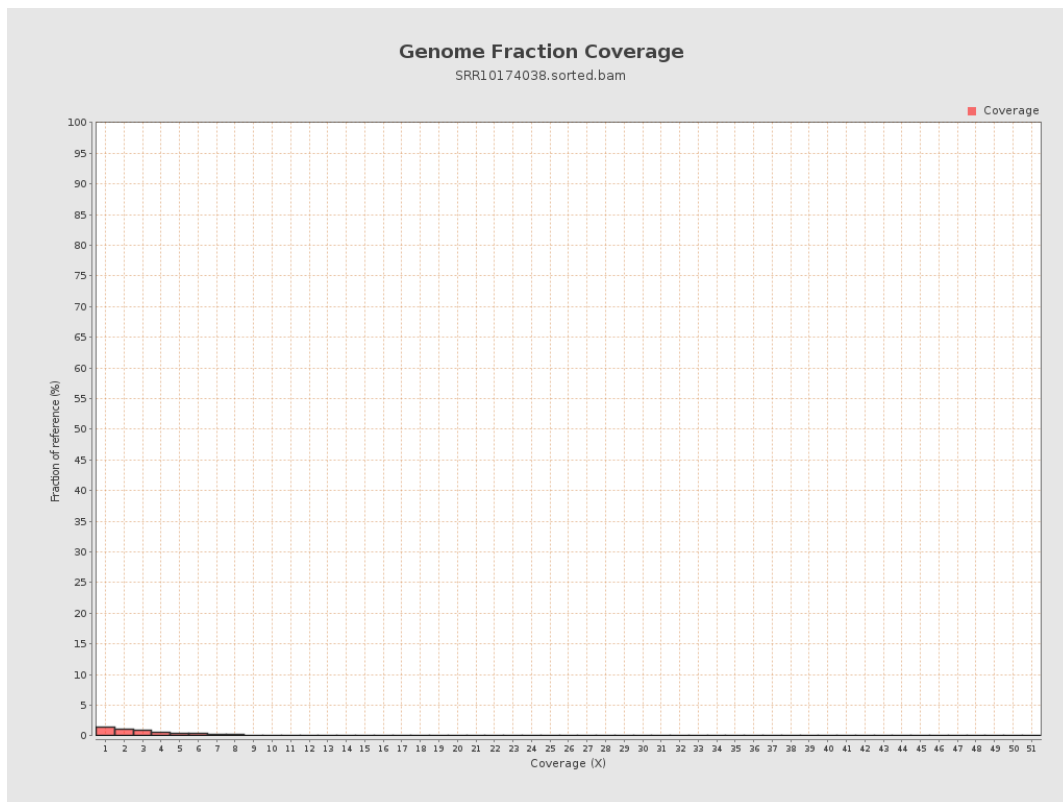
4. Results : Coverage Histogram



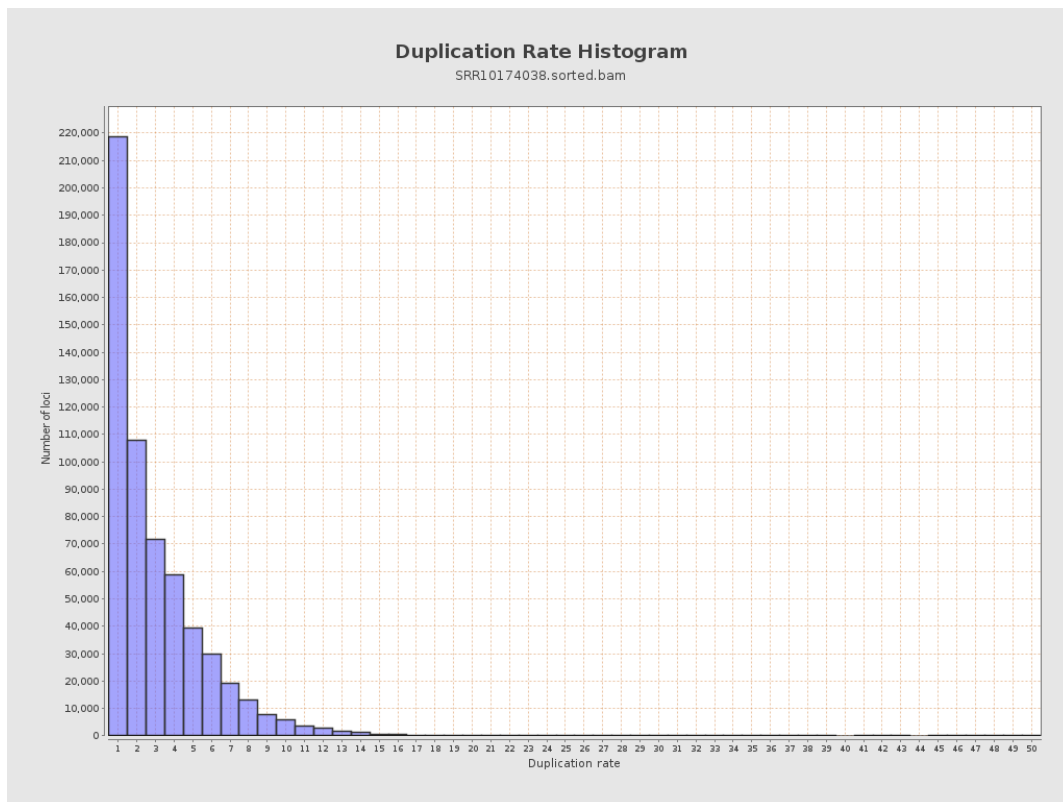
5. Results : Coverage Histogram (0-50X)



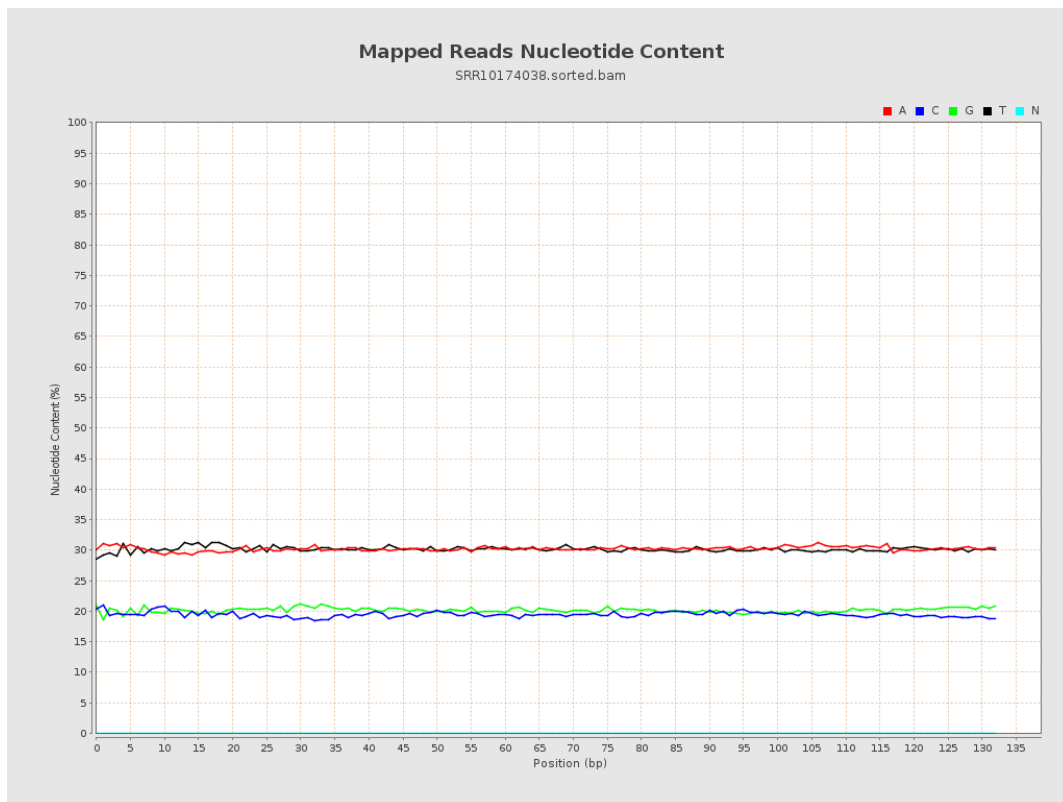
6. Results : Genome Fraction Coverage



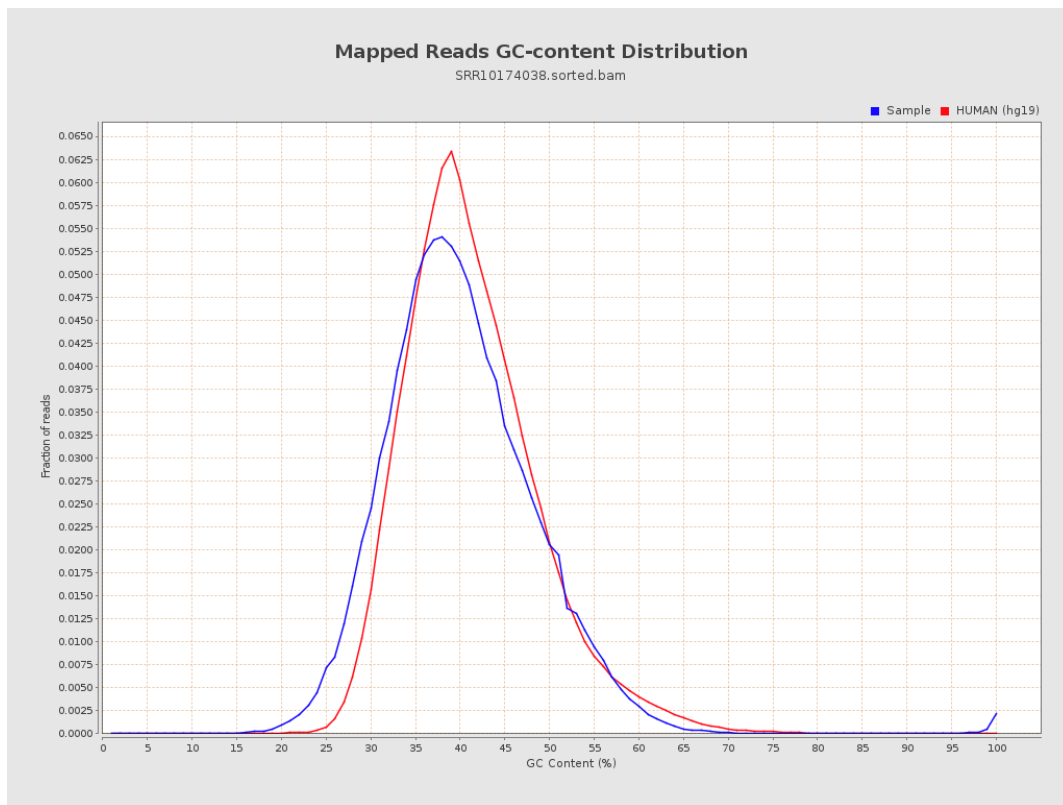
7. Results : Duplication Rate Histogram



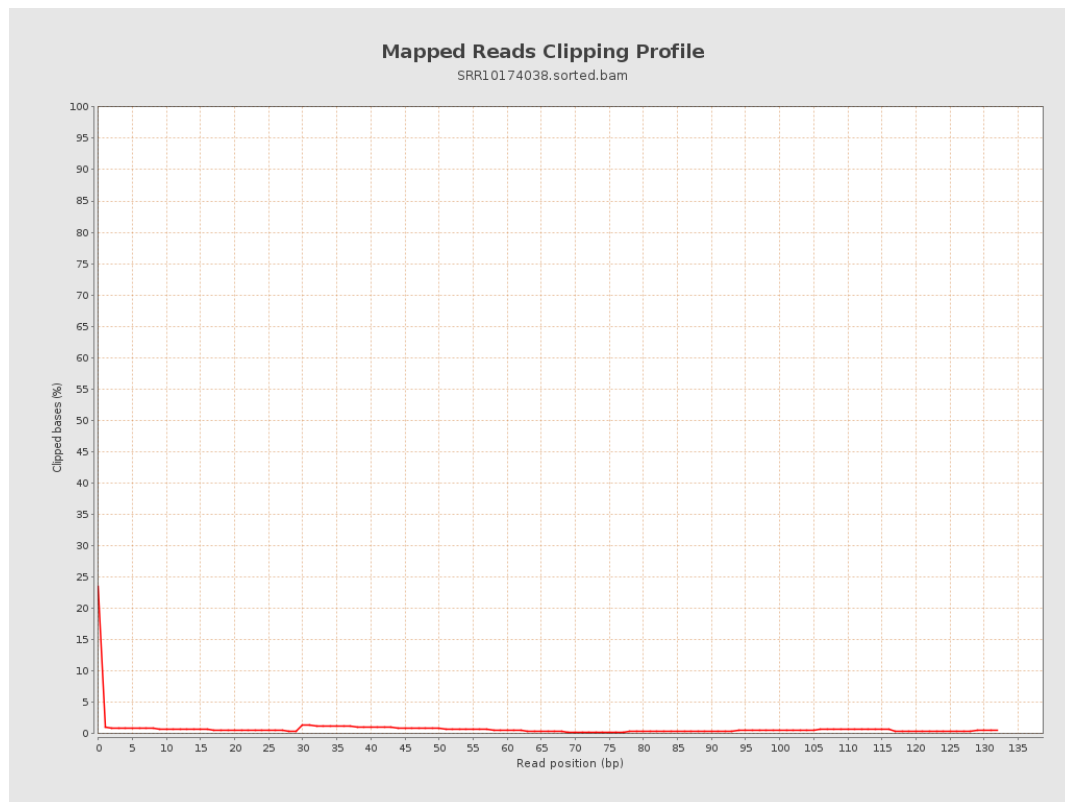
8. Results : Mapped Reads Nucleotide Content



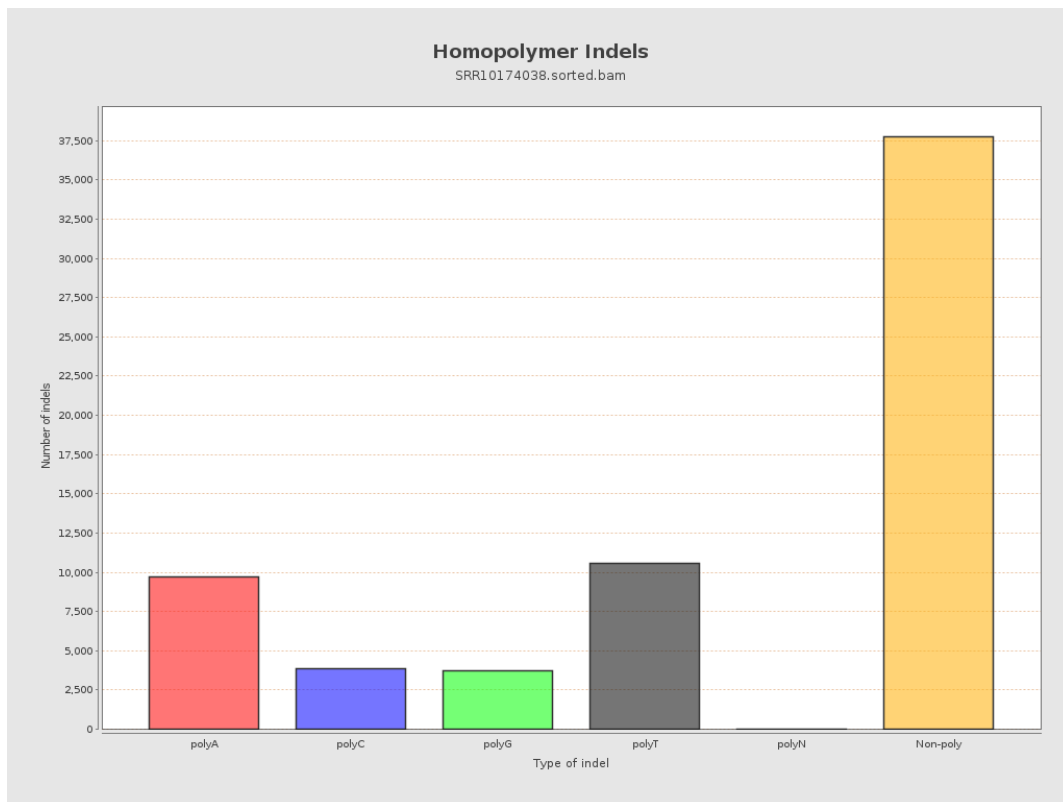
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



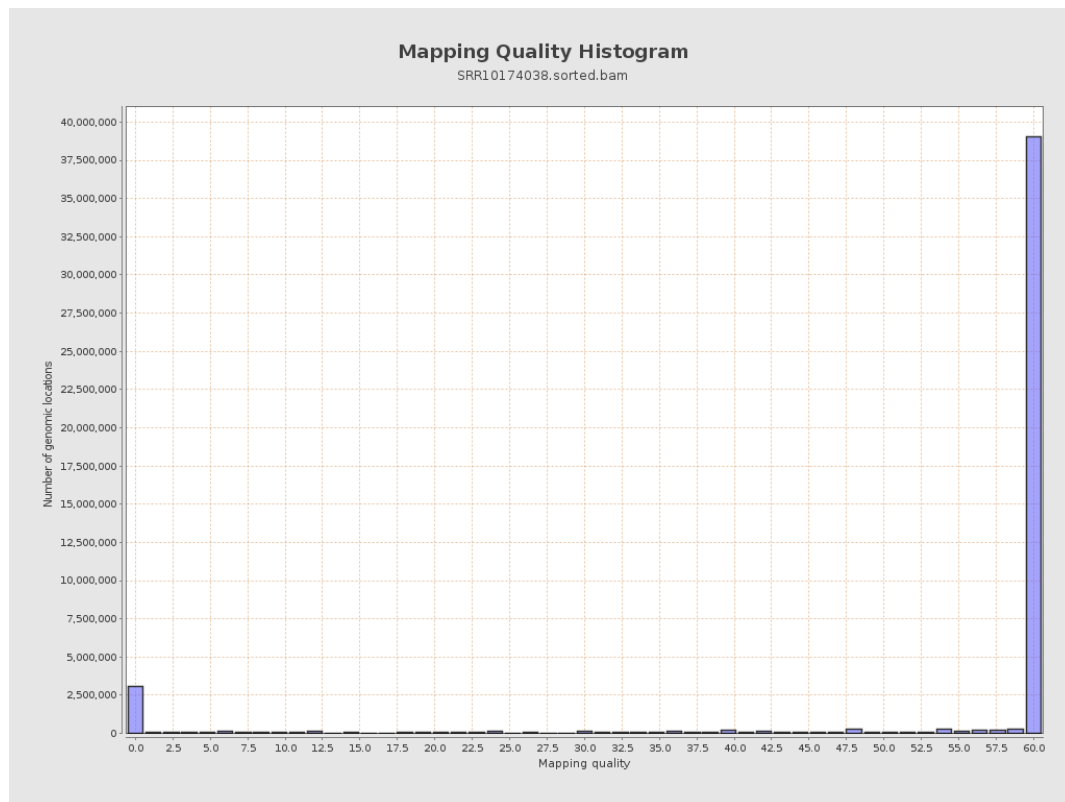
11. Results : Homopolymer Indels



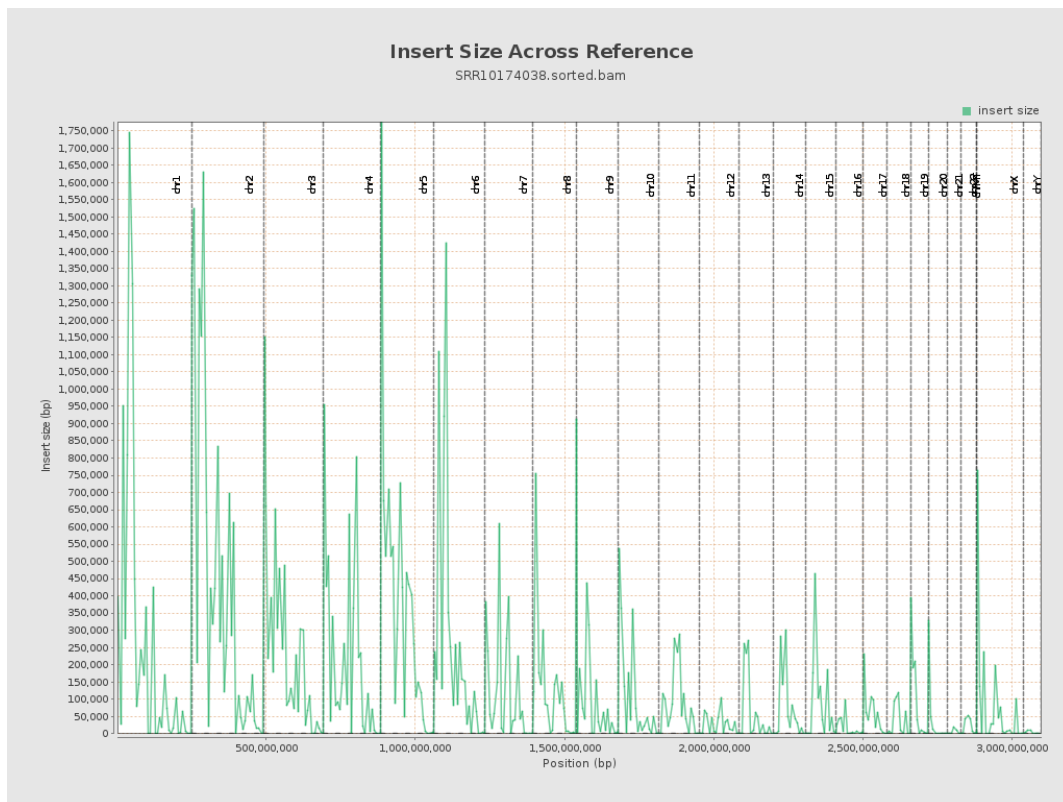
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

